

# Wei Chen

## List of Publications by Year in descending order

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136  
papers

24,232  
citations

61857

43  
h-index

13727

129  
g-index

151  
all docs

151  
docs citations

151  
times ranked

45901  
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	A genome-wide association study of global gene expression. <i>Nature Genetics</i> , 2007, 39, 1202-1207.	9.4	882
3	Seven new loci associated with age-related macular degeneration. <i>Nature Genetics</i> , 2013, 45, 433-439.	9.4	687
4	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	3.3	589
5	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , 2011, 43, 712-714.	9.4	525
6	Genetic variants near <i>TIMP3</i> and high-density lipoprotein-associated loci influence susceptibility to age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7401-7406.	3.3	475
7	Proliferating SPP1/MERTK-expressing macrophages in idiopathic pulmonary fibrosis. <i>European Respiratory Journal</i> , 2019, 54, 1802441.	3.1	400
8	A variant of mitochondrial protein LOC387715/ARMS2, not HTRA1, is strongly associated with age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16227-16232.	3.3	398
9	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. <i>American Journal of Human Genetics</i> , 2016, 98, 653-666.	2.6	347
10	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462.	9.0	308
11	Adaptive plasticity of IL-10 <sup>+</sup> and IL-35 <sup>+</sup> Treg cells cooperatively promotes tumor T cell exhaustion. <i>Nature Immunology</i> , 2019, 20, 724-735.	7.0	297
12	Transcriptome analysis and molecular signature of human retinal pigment epithelium. <i>Human Molecular Genetics</i> , 2010, 19, 2468-2486.	1.4	249
13	E2-2 Protein and Fuchs's Corneal Dystrophy. <i>New England Journal of Medicine</i> , 2010, 363, 1016-1024.	13.9	247
14	SFRP2/DPP4 and FMO1/LSP1 Define Major Fibroblast Populations in Human Skin. <i>Journal of Investigative Dermatology</i> , 2018, 138, 802-810.	0.3	236
15	Treg Cells Promote the SREBP1-Dependent Metabolic Fitness of Tumor-Promoting Macrophages via Repression of CD8 <sup>+</sup> T Cell-Derived Interferon- $\gamma$ . <i>Immunity</i> , 2019, 51, 381-397.e6.	6.6	186
16	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011, 12, R84.	13.9	173
17	Gene Expression in Skin and Lymphoblastoid Cells: Refined Statistical Method Reveals Extensive Overlap in cis-eQTL Signals. <i>American Journal of Human Genetics</i> , 2010, 87, 779-789.	2.6	169
18	Genetic susceptibility to age-related macular degeneration: a paradigm for dissecting complex disease traits. <i>Human Molecular Genetics</i> , 2007, 16, R174-R182.	1.4	168

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19	DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. <i>Lancet Respiratory Medicine</i> , 2019, 7, 336-346.	5.2	147
20	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013, 22, 1663-1678.	1.4	141
21	Evidence of association of <i>APOE</i> with age-related macular degeneration - a pooled analysis of 15 studies. <i>Human Mutation</i> , 2011, 32, 1407-1416.	1.1	130
22	IL-17 Receptor Signaling in the Lung Epithelium Is Required for Mucosal Chemokine Gradients and Pulmonary Host Defense against <i>K. pneumoniae</i> . <i>Cell Host and Microbe</i> , 2016, 20, 596-605.	5.1	115
23	The Influence of Age and Sex on Ocular Surface Microbiota in Healthy Adults. , 2017, 58, 6030.		107
24	Myofibroblast transcriptome indicates SFRP2hi fibroblast progenitors in systemic sclerosis skin. <i>Nature Communications</i> , 2021, 12, 4384.	5.8	101
25	Stress and Bronchodilator Response in Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 47-56.	2.5	99
26	<i>ADCYAP1R1</i> and Asthma in Puerto Rican Children. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 584-588.	2.5	97
27	Genome-wide association study and meta-analysis of intraocular pressure. <i>Human Genetics</i> , 2014, 133, 41-57.	1.8	93
28	Complement Factor D in Age-Related Macular Degeneration. , 2011, 52, 8828.		92
29	PIRs mediate innate myeloid cell memory to nonself MHC molecules. <i>Science</i> , 2020, 368, 1122-1127.	6.0	92
30	A Bayesian framework for <i>de novo</i> mutation calling in parents-offspring trios. <i>Bioinformatics</i> , 2015, 31, 1375-1381.	1.8	87
31	Variations in Apolipoprotein E Frequency With Age in a Pooled Analysis of a Large Group of Older People. <i>American Journal of Epidemiology</i> , 2011, 173, 1357-1364.	1.6	85
32	AIM2 Inflammasome Is Critical for Influenza-Induced Lung Injury and Mortality. <i>Journal of Immunology</i> , 2017, 198, 4383-4393.	0.4	85
33	Deep-learning-based prediction of late age-related macular degeneration progression. <i>Nature Machine Intelligence</i> , 2020, 2, 141-150.	8.3	79
34	A Likelihood-Based Framework for Variant Calling and De Novo Mutation Detection in Families. <i>PLoS Genetics</i> , 2012, 8, e1002944.	1.5	71
35	A systematic study of normalization methods for Infinium 450K methylation data using whole-genome bisulfite sequencing data. <i>Epigenetics</i> , 2015, 10, 662-669.	1.3	68
36	DIMM-SC: a Dirichlet mixture model for clustering droplet-based single cell transcriptomic data. <i>Bioinformatics</i> , 2018, 34, 139-146.	1.8	68

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37	Genome-wide analysis of disease progression in age-related macular degeneration. <i>Human Molecular Genetics</i> , 2018, 27, 929-940.	1.4	67
38	EZH2 and ALDH-1 mark breast epithelium at risk for breast cancer development. <i>Modern Pathology</i> , 2011, 24, 786-793.	2.9	66
39	FastGGM: An Efficient Algorithm for the Inference of Gaussian Graphical Model in Biological Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1004755.	1.5	63
40	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. <i>Nature Communications</i> , 2019, 10, 1649.	5.8	56
41	Nasal DNA methylation profiling of asthma and rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1655-1663.	1.5	56
42	Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing. , 2017, 58, 128.		55
43	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 3248-3260.	2.7	55
44	An epigenome-wide association study of total serum IgE in Hispanic children. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 571-577.	1.5	53
45	A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. <i>European Respiratory Journal</i> , 2017, 49, 1601505.	3.1	51
46	Oncological outcome of T1 rectal cancer undergoing standard resection and local excision. <i>Colorectal Disease</i> , 2011, 13, e14-e19.	0.7	50
47	BREM-SC: a bayesian random effects mixture model for joint clustering single cell multi-omics data. <i>Nucleic Acids Research</i> , 2020, 48, 5814-5824.	6.5	50
48	A 32 kb Critical Region Excluding Y402H in CFH Mediates Risk for Age-Related Macular Degeneration. <i>PLoS ONE</i> , 2011, 6, e25598.	1.1	46
49	Genotype calling and haplotyping in parent-offspring trios. <i>Genome Research</i> , 2013, 23, 142-151.	2.4	46
50	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. <i>Genetics</i> , 2017, 206, 119-133.	1.2	46
51	Association between CFH Y402H Polymorphism and Age Related Macular Degeneration in North Indian Cohort. <i>PLoS ONE</i> , 2013, 8, e70193.	1.1	42
52	A Genome-Wide Association Study of Chronic Obstructive Pulmonary Disease in Hispanics. <i>Annals of the American Thoracic Society</i> , 2015, 12, 340-348.	1.5	41
53	Age-related macular degeneration-associated variants at chromosome 10q26 do not significantly alter ARMS2 and HTRA1 transcript levels in the human retina. <i>Molecular Vision</i> , 2010, 16, 1317-23.	1.1	40
54	Single cell RNA sequencing identifies an early monocyte gene signature in acute respiratory distress syndrome. <i>JCI Insight</i> , 2020, 5, .	2.3	39

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55	CXXC finger protein 1 is critical for T-cell intrathymic development through regulating H3K4 trimethylation. <i>Nature Communications</i> , 2016, 7, 11687.	5.8	38
56	Cell-Deposited Matrix Improves Retinal Pigment Epithelium Survival on Aged Submacular Human Bruch's Membrane. , 2011, 52, 1345.		37
57	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 208-219.	2.5	37
58	GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. <i>Genome Biology</i> , 2020, 21, 188.	3.8	37
59	SILGGM: An extensive R package for efficient statistical inference in large-scale gene networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006369.	1.5	33
60	High-dimensional profiling clusters asthma severity by lymphoid and non-lymphoid status. <i>Cell Reports</i> , 2021, 35, 108974.	2.9	32
61	Deficiency in AIM2 induces inflammation and adipogenesis in white adipose tissue leading to obesity and insulin resistance. <i>Diabetologia</i> , 2019, 62, 2325-2339.	2.9	31
62	Serum Cadmium and Lead, Current Wheeze, and Lung Function in a Nationwide Study of Adults in the United States. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2019, 7, 2653-2660.e3.	2.0	29
63	Geographic Difference Shaped Human Ocular Surface Metagenome of Young Han Chinese From Beijing, Wenzhou, and Guangzhou Cities. , 2020, 61, 47.		29
64	A road map from single-cell transcriptome to patient classification for the immune response to trauma. <i>JCI Insight</i> , 2021, 6, .	2.3	29
65	Expression Quantitative Trait Methylation Analysis Reveals Methylomic Associations With Gene Expression in Childhood Asthma. <i>Chest</i> , 2020, 158, 1841-1856.	0.4	28
66	SNP@Evolution: a hierarchical database of positive selection on the human genome. <i>BMC Evolutionary Biology</i> , 2009, 9, 221.	3.2	26
67	Prognostic analysis for carcinoid tumours of the rectum: a single institutional analysis of 106 patients. <i>Colorectal Disease</i> , 2011, 13, 150-153.	0.7	26
68	A Multiomics Approach to Identify Genes Associated with Childhood Asthma Risk and Morbidity. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 439-447.	1.4	26
69	Genome-wide association study-based deep learning for survival prediction. <i>Statistics in Medicine</i> , 2020, 39, 4605-4620.	0.8	26
70	Glycated Hemoglobin A1c, Lung Function, and Hospitalizations Among Adults with Asthma. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2020, 8, 3409-3415.e1.	2.0	26
71	Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. <i>Genetics</i> , 2015, 200, 1089-1104.	1.2	25
72	Genome-wide interaction study of dust mite allergen on lung function in children with asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 996-1003.e7.	1.5	25

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73	Long-Term Outcome of Early-Stage Rectal Cancer Undergoing Standard Resection and Local Excision. <i>Clinical Colorectal Cancer</i> , 2011, 10, 37-41.	1.0	23
74	Native American Ancestry, Lung Function, and COPD in Costa Ricans. <i>Chest</i> , 2014, 145, 704-710.	0.4	23
75	Transcriptomic Responses to Ivacaftor and Prediction of Ivacaftor Clinical Responsiveness. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 643-652.	1.4	23
76	A genome-wide association study of asthma hospitalizations in adults. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 933-940.	1.5	23
77	Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. <i>Pediatric Pulmonology</i> , 2021, 56, 1896-1905.	1.0	22
78	Antiinflammatory effects of bromodomain and extraterminal domain inhibition in cystic fibrosis lung inflammation. <i>JCI Insight</i> , 2016, 1, .	2.3	21
79	SNPs identified by GWAS affect asthma risk through DNA methylation and expression of cis-genes in airway epithelium. <i>European Respiratory Journal</i> , 2020, 55, 1902079.	3.1	21
80	Variants in oxidative stress-related genes affect the chemosensitivity through Nrf2-mediated signaling pathway in biliary tract cancer. <i>EBioMedicine</i> , 2019, 48, 143-160.	2.7	20
81	Transcriptomics of atopy and atopic asthma in white blood cells from children and adolescents. <i>European Respiratory Journal</i> , 2019, 53, 1900102.	3.1	20
82	DISSCO: direct imputation of summary statistics allowing covariates. <i>Bioinformatics</i> , 2015, 31, 2434-2442.	1.8	18
83	Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. <i>Genetics</i> , 2016, 202, 457-470.	1.2	18
84	A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 634-637.	2.5	16
85	Statistics for X-chromosome associations. <i>Genetic Epidemiology</i> , 2018, 42, 539-550.	0.6	16
86	Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 671-675.	1.5	16
87	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <i>Statistics in Biosciences</i> , 2013, 5, 3-25.	0.6	15
88	Bayesian integrative model for multi-omics data with missingness. <i>Bioinformatics</i> , 2018, 34, 3801-3808.	1.8	15
89	Sleep Duration, Current Asthma, and Lung Function in a Nationwide Study of U.S. Adults. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 926-929.	2.5	15
90	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. <i>European Respiratory Journal</i> , 2021, 57, 2002693.	3.1	15

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91	Integration of genetic signature and TNM staging system for predicting the relapse of locally advanced colorectal cancer. <i>International Journal of Colorectal Disease</i> , 2010, 25, 1277-1285.	1.0	14
92	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. <i>Bioinformatics</i> , 2015, 31, 1452-1459.	1.8	14
93	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. <i>Genetics</i> , 2015, 201, 1329-1339.	1.2	14
94	Pancreatic gene expression during recovery after pancreatitis reveals unique transcriptome profiles. <i>Scientific Reports</i> , 2018, 8, 1406.	1.6	14
95	Copula-based score test for bivariate time-to-event data, with application to a genetic study of AMD progression. <i>Lifetime Data Analysis</i> , 2019, 25, 546-568.	0.4	14
96	Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. <i>Translational Vision Science and Technology</i> , 2021, 10, 29.	1.1	14
97	Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. <i>Genetic Epidemiology</i> , 2016, 40, 133-143.	0.6	12
98	The impact of genotype calling errors on family-based studies. <i>Scientific Reports</i> , 2016, 6, 28323.	1.6	12
99	RNA-seq in Pulmonary Medicine: How Much Is Enough?. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 389-391.	2.5	11
100	Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. <i>Epigenetics</i> , 2016, 11, 132-139.	1.3	10
101	Artificial-cell-type aware cell-type classification in CITE-seq. <i>Bioinformatics</i> , 2020, 36, i542-i550.	1.8	10
102	A genome-wide study of DNA methylation in white blood cells and asthma in Latino children and youth. <i>Epigenetics</i> , 2021, 16, 577-585.	1.3	10
103	Expression Quantitative Trait Loci (eQTL) Mapping in Puerto Rican Children. <i>PLoS ONE</i> , 2015, 10, e0122464.	1.1	10
104	Using Current Data to Define New Approach in Age Related Macular Degeneration: Need to Accelerate Translational Research. <i>Current Genomics</i> , 2014, 15, 266-277.	0.7	10
105	Robust and accurate estimation of cellular fraction from tissue omics data via ensemble deconvolution. <i>Bioinformatics</i> , 2022, 38, 3004-3010.	1.8	10
106	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. <i>Human Heredity</i> , 2015, 80, 126-138.	0.4	9
107	KMgene: a unified R package for gene-based association analysis for complex traits. <i>Bioinformatics</i> , 2018, 34, 2144-2146.	1.8	9
108	The Genetic Variant on Chromosome 10p14 Is Associated with Risk of Colorectal Cancer: Results from a Case-Control Study and a Meta-Analysis. <i>PLoS ONE</i> , 2013, 8, e64310.	1.1	9

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109	CWAS GUI: graphical browser for the results of whole-genome association studies with high-dimensional phenotypes. <i>Bioinformatics</i> , 2009, 25, 284-285.	1.8	8
110	A computational method for genotype calling in family-based sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 37.	1.2	8
111	Association of <i>IGFN1</i> variant with polypoidal choroidal vasculopathy. <i>Journal of Gene Medicine</i> , 2018, 20, e3007.	1.4	8
112	Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. <i>BMC Cancer</i> , 2019, 19, 686.	1.1	8
113	Child maltreatment, anxiety and depression, and asthma among British adults in the UK Biobank. <i>European Respiratory Journal</i> , 2022, 60, 2103160.	3.1	8
114	The independent prognostic value of global epigenetic alterations: An analysis of single-cell ATAC-seq of circulating leukocytes from trauma patients followed by validation in whole blood leukocyte transcriptomes across three etiologies of critical illness. <i>EBioMedicine</i> , 2022, 76, 103860.	2.7	7
115	LONGL-Net: temporal correlation structure guided deep learning model to predict longitudinal age-related macular degeneration severity. , 2022, 1, pgab003.		7
116	Gene-based association analysis for bivariate time-to-event data through functional regression with copula models. <i>Biometrics</i> , 2020, 76, 619-629.	0.8	6
117	AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1256, 191-200.	0.8	6
118	LAIT: a local ancestry inference toolkit. <i>BMC Genetics</i> , 2017, 18, 83.	2.7	5
119	Differential gene expression in nasal airway epithelium from overweight or obese youth with asthma. <i>Pediatric Allergy and Immunology</i> , 2022, 33, e13776.	1.1	5
120	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. <i>European Journal of Human Genetics</i> , 2017, 25, 350-359.	1.4	4
121	A region-based method for causal mediation analysis of DNA methylation data. <i>Epigenetics</i> , 2022, 17, 286-296.	1.3	4
122	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. <i>PLoS Genetics</i> , 2015, 11, e1005271.	1.5	3
123	A Pipeline for Classifying Relationships Using Dense SNP/SNV Data and Putative Pedigree Information. <i>Genetic Epidemiology</i> , 2016, 40, 161-171.	0.6	3
124	A semiparametric imputation approach for regression with censored covariate with application to an AMD progression study. <i>Statistics in Medicine</i> , 2018, 37, 3293-3308.	0.8	3
125	Clinical utility of ultrahigh fractional exhaled nitric oxide in predicting bronchial hyperresponsiveness in patients with suspected asthma. <i>Postgraduate Medical Journal</i> , 2019, 95, 541-546.	0.9	3
126	Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells. <i>Epigenetics</i> , 2019, 14, 844-849.	1.3	3



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127	An integrative association method for omics data based on a modified Fisher's method with application to childhood asthma. <i>PLoS Genetics</i> , 2019, 15, e1008142.	1.5	3
128	Under-diagnosis of atopic dermatitis in Puerto Rican children. <i>World Allergy Organization Journal</i> , 2019, 12, 100003.	1.6	3
129	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. <i>Journal of the American Statistical Association</i> , 2021, 116, 531-545.	1.8	3
130	CSMD: a computational subtraction-based microbiome discovery pipeline for species-level characterization of clinical metagenomic samples. <i>Bioinformatics</i> , 2019, 36, 1577-1583.	1.8	2
131	Identification and inference for subgroups with differential treatment efficacy from randomized controlled trials with survival outcomes through multiple testing. <i>Statistics in Medicine</i> , 2021, 40, 6523-6540.	0.8	2
132	Rapid reconstitution of regulatory T-cell subsets is associated with reduced rates of acute graft-versus-host disease and absence of viremia after cord blood transplantation in children with reduced-intensity conditioning using alemtuzumab. <i>Cytotherapy</i> , 2020, 22, 149-157.	0.3	1
133	Inference of large modified Poisson-type graphical models: Application to RNA-seq data in childhood atopic asthma studies. <i>Annals of Applied Statistics</i> , 2021, 15, .	0.5	1
134	DNA Methylation and Atopic Diseases. <i>Methods in Molecular Biology</i> , 2022, 2432, 85-99.	0.4	1
135	CHIT: an allele-specific method for testing the association between molecular quantitative traits and phenotype-genotype interaction. <i>Bioinformatics</i> , 2021, 37, 4764-4770.	1.8	0
136	A Genome-wide Study of DNA Methylation in Nasal Epithelium and Atopy and Atopic Asthma in Children. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0